



THIRD SUBSTITUTE SEQUENCE LISTING

<110> Thompson, M. Craig
Long, Fan
Wobbe, C. Richard

<120> A NOVEL FUNGAL MULTISUBUNIT PROTEIN
COMPLEX CRITICAL FOR EXPRESSION OF FUNGAL PROTEINS

<130> 0342/1D516US2

<140> US 09/601,965

<141> 2000-10-20

<150> PCT/US99/02940

<151> 1999-02-08

<150> 60/074,100

<151> 1998-02-09

<160> 32

<170> FastSEQ for Windows Version 3.0

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<211> 4116

<212> DNA

<213> C. albicans

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<213> C. albicans

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			20					25					30		
Arg	Leu	Leu	Gln	Glu	Gly	Gln	Pro	Glu	Leu	Thr	Asn	Asp	Glu	Glu	Met
			35				40					45			
Ala	Ala	Gln	Ala	Ala	Ala	Glu	Ser	Gln	Phe	Asp	Ala	Leu	Phe	Gly	Asn
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 Asp Asp Asn Asp Gly Leu Asn Asp Leu Gly Glu Leu Phe Asp Asp Gln
 115 120 125
 Gln Glu Asp Ser Asn Val Ile Asn Thr Lys Lys His Lys Leu Asp Asp
 130 135 140
 Asp Ser Asn Asn Asp Gly Lys Thr Ala Gln Glu Asp Gln Lys Glu Lys
 145 150 155 160
 Glu Asn Lys Arg Gln Leu Lys Arg Gln Lys Leu Gln Lys Ile Val Lys
 165 170 175
 His Leu Glu Lys Glu Gln Ile Lys Arg Asn Ile Lys Tyr Tyr Phe Pro
 180 185 190
 Thr Tyr Ser Arg His Arg Pro Phe Asn Phe His Lys Phe Phe Ser Pro
 195 200 205
 Ser Pro Gln Tyr Tyr Arg Tyr Gln Arg Pro Ala Ile Ala Leu Ser Lys
 210 215 220
 Asn Ile Lys Pro Leu Ile Pro Thr Lys Val Asn Leu Glu Ile Glu Val
 225 230 235 240
 Asp Gln Lys Lys Ile Phe Lys Leu Arg Ser Ala Asp Thr Ala Ser Leu
 245 250 255
 Ser His Glu Asp Lys Asn Val Thr Asn Ile Thr Gln Asp Asp Leu Asp
 260 265 270
 Phe Ile Lys Asn Leu Glu Ser Lys Arg Ser Ser Ile Asp Ser Phe Ile
 275 280 285
 Lys Glu Ile Asp Tyr Val Lys Arg Asp Trp Thr Asn Cys Asp Lys Phe
 290 295 300
 Asp His Tyr Ser Lys Asp Leu Val Leu Ser Thr Thr Asp Trp Asp Asp
 305 310 315 320
 Asp Ala Ile Ile Asn Ala Gly Asp Asn Glu Tyr Ser Ile Val Lys Pro
 325 330 335
 Ile Asn Glu Leu Leu Leu Asn Asn Pro Leu Asp Asn Ser Lys Gln Asn
 340 345 350
 Arg Gln Lys Ile Glu Asn Asp Asn Thr Thr Asn Asn Tyr Asn Gln Asn
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 Asn Ser Asn Val Gln Asp Glu Glu Glu Asp Asp Asp Ile Phe Asn Gly
 370 375 380
 Gln Ile Asn Leu Asp Lys Leu Lys Leu Asp Met Asn Asp Pro Asn Leu
 385 390 395 400
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 405 410 415
 Ser Thr Asp Lys Leu Leu Glu Leu Lys Phe Asn Ile Ser Asn Asp Gln
 420 425 430
 Glu Tyr Glu Leu Leu Arg Lys Asn Tyr Asn Thr Lys Gln Arg Ser Gln
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 Leu Ser Asn Leu Asn Ile Glu His Ser Val Pro Ala Leu Arg Leu Gln
 450 455 460
 Thr Pro Tyr Tyr Lys Val Lys Leu Ser Thr Asp Glu Thr Arg Ser Phe
 465 470 475 480
 His Arg Pro Val Phe Asn Val Arg Pro Gly Thr Leu Val Ser Phe Ser
 485 490 495
 Lys Leu Lys Leu Arg Lys Arg Lys Lys Asp Lys Gly Lys Ser Leu Gln
 500 505 510
 Gln Ile Phe Ser Lys Thr Ser Asp Leu Thr Val Ala Asp Thr Gly Asn

PL
 C. G.

Ile	Ile	Ala	Leu	Glu	Tyr	Ser	Glu	Gln	Tyr	Pro	Pro	Ile	Leu	Ser	Asn
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Phe	Gly	Met	Gly	Ser	Lys	Leu	Ile	Asn	Tyr	Tyr	Arg	Lys	Glu	Arg	Pro
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Asn	Asp	Thr	Ser	Arg	Pro	Lys	Ala	Gln	Ile	Gly	Glu	Thr	His	Ile	Leu
				565					570					575	
Gly	Val	Glu	Asp	Arg	Ser	Pro	Phe	Trp	Asn	Phe	Gly	Glu	Val	Ala	Pro
			580					585					590		
Gly	Asp	Phe	Val	Pro	Thr	Leu	Tyr	Asn	Asn	Met	Val	Arg	Ala	Pro	Ile
		595				600						605			
Phe	Lys	His	Asp	Asn	Lys	Pro	Thr	Asp	Phe	Leu	Leu	Val	Lys	Ser	Gln
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Gly	Ala	Gly	Ser	His	Gln	Lys	Phe	Tyr	Leu	Arg	Gly	Ile	Asn	Phe	Asn
625					630					635					640
Phe	Ala	Val	Gly	Asn	Thr	Phe	Pro	Val	Glu	Val	Pro	Ala	Pro	His	Ser
				645					650					655	
Arg	Lys	Val	Thr	Asn	Ile	Ser	Lys	Asn	Arg	Leu	Lys	Met	Val	Val	Phe
			660					665					670		
Arg	Val	Met	Asn	Ser	Leu	Gly	Val	Pro	Arg	Ile	Ser	Val	Lys	Asp	Val
		675				680						685			
Ser	Lys	His	Phe	Pro	Glu	His	Ser	Asp	Met	Gln	Asn	Arg	Gln	Arg	Leu
	690					695					700				
Lys	Glu	Phe	Met	Glu	Tyr	Gln	Arg	Gln	Gly	Glu	Asp	Gln	Gly	Tyr	Trp
705					710					715					720
Lys	Val	Arg	Gly	Leu	Asn	Asp	Val	Ile	Pro	Gly	Glu	Glu	Glu	Ile	Arg
				725					730					735	
Thr	Met	Ile	Thr	Pro	Glu	Asp	Ser	Ser	Leu	Met	Asp	Thr	Met	Gln	Phe
			740					745					750		
Gly	Gln	Gln	Val	Leu	Asp	Asp	Asn	Met	Val	Leu	Phe	Gly	Glu	Gln	Ser
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	770					775					780				
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Lys	Glu	Val	Glu	Lys	Glu	Lys	Glu	Gln	Glu	Arg	Glu	Glu	Glu	Lys	Gly
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			820					825					830		
Glu	Lys	Ser	Lys	Lys	Ser	Lys	Glu	Gln	Asp	Thr	Glu	Ile	Asp	Val	Glu
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Glu	Glu	Leu	Ala	Pro	Trp	Asn	Leu	Ser	Arg	Asn	Phe	Val	Ile	Ala	Asn
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Gln	Thr	Lys	Thr	Met	Leu	Gln	Leu	Asn	Gly	Glu	Gly	Asp	Pro	Thr	Gly
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 Gln Asn Arg Val Leu Arg Ile Thr Arg Arg Val Arg Asp Glu Asn Gly
 995 1000 1005
 Ile Val His Arg Lys Val Glu Phe Ile His Asp Pro Arg Leu Ile Arg
 1010 1015 1020
 Ala Tyr Val Lys Arg Lys Lys Gln Ile Glu Asp Glu Leu Leu Lys Asn
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 Ala Lys Gln Ser Arg Ala Lys Lys Pro Pro Lys Asp Leu Ile His Ala
 1075 1080 1085
 Ala Ala Ala Ala Gly Ala Thr Ile Ile Asp Ala Asn Thr Val Met Leu
 1090 1095 1100
 Pro Asp Gly Ser Tyr Val Ile Gly Gly Lys Gly Ile Gly Lys Gly Lys
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 Ser Arg Thr Arg Arg Cys Lys Asn Cys Gly Ala Tyr Gly His Ile Arg
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 Glu His Leu Pro Asp Ala Val Asp Phe Glu Asp Glu Asp Glu Leu Ala
 50 55 60
 Asp Asp Asp Asp Asp Leu Pro Glu Glu Ser Asp Ala Asn Leu His Pro
 65 70 75 80
 Ala Met Met Thr Met Gly Ala Tyr Asp Asp Val Asn Glu Asn Gly Ala
 85 90 95
 Val Leu Gly Ile Asp Ser Asn Ser Leu Asn Met Gln Leu Pro Glu Ile
 100 105 110
 Asn Gly Asp Leu Ser Gln Gln Phe Ile Leu Glu Asp Asp Gly Gly Thr
 115 120 125
 Pro Ala Thr Ser Asn Ala Leu Phe Met Gly Met Asp Ala Asn Glu Ile
 130 135 140
 His Leu Ala Thr Glu Thr Gly Val Leu Asp Gly Ser Gly Ala Asn Glu
 145 150 155 160
 Ile Gly His Ser Gln Leu Ser Ile Gly Gly Val Asn Gly Asn Asp Met
 165 170 175
 Ser Ile Asn Gly Gly Phe Ile Met Glu Pro Asp Met Ser Asp Gly Lys
 180 185 190
 His Lys Lys Ala Thr Lys Leu Asp Leu Ile Asn His Glu Lys Tyr Leu
 195 200 205

Leu Lys Lys Tyr Phe Pro Asp Phe Glu Lys Gly Lys Ile Leu Lys Trp
 210 215 220
 Asn Lys Leu Ile Tyr Arg Arg Ser Val Pro Tyr His Trp His Ser Glu
 225 230 235 240
 Ile Ser Arg Val Lys Lys Pro Phe Met Pro Leu Asn Leu Lys Phe Lys
 245 250 255
 Val Gln Gln Asp Asp Lys Arg Leu Phe Asn Ser Arg Thr Ile Ser Tyr
 260 265 270
 Val Ala Pro Ile Tyr Gln Gly Lys Asn Asn Leu Leu Gln Ser Asn Ser
 275 280 285
 Ser Ala Ser Arg Arg Gly Leu Ile His Val Ser Ile Asp Glu Leu Phe
 290 295 300
 Pro Ile Lys Glu Gln Gln Lys Lys Arg Lys Ile Ile His Asp Glu Lys
 305 310 315 320
 Thr Ile Ser Glu Asp Leu Leu Ile Ala Thr Asp Asp Trp Asp Gln Glu
 325 330 335
 Lys Ile Ile Asn Gln Gly Thr Ser Ser Thr Ala Thr Leu Ala Asp Ser
 340 345 350
 Ser Met Thr Pro Asn Leu Lys Phe Ser Gly Gly Tyr Lys Leu Lys Ser
 355 360 365
 Leu Ile Glu Asp Val Ala Glu Asp Trp Gln Trp Asp Glu Asp Met Ile
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 Ile Asp Ala Lys Leu Lys Glu Ser Lys His Ala Glu Leu Asn Met Asn
 385 390 395 400
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 405 410 415
 Gln Lys Gln Gln Leu Asp Ser Ser Asn Leu Ile Leu Pro Leu Asn Glu
 420 425 430
 Thr Ile Leu Gln Gln Lys Phe Asn Leu Ser Asn Asp Asp Lys Tyr Gln
 435 440 445
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 450 455 460
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 Tyr Lys Val Ala Val Pro Arg Tyr Gln Leu Arg His Phe His Arg Glu
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 Val Gln Asp Lys Ser Pro Phe Trp Asn Phe Gly Phe Val Glu Pro Gly
 595 600 605
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Met	Asn	Glu	Ser	Pro	Lys	Ile	Leu	Asp	Ser	Ser	Phe	Glu	Asn	Ser	Asn	50	55	60	
Pro	Gln	Asp	Gly	Pro	Asn	Tyr	Glu	Asp	Phe	Asp	Phe	Met	Gly	Ser	Ile	65	70	75	80
His	Lys	Glu	Phe	Gly	Asn	Asn	Ile	Asn	Glu	Met	Asp	Asp	Met	Glu	Asp	85	90	95	
Val	Ser	Asp	Asp	Asn	Leu	Pro	Glu	Glu	Gln	Ala	Val	Asn	Tyr	Thr		100	105	110	
Gly	Asp	Lys	Asp	Asp	Glu	Asp	Phe	Gly	Lys	Leu	Leu	Ala	Lys	Glu	Met	115	120	125	
Gly	Glu	Glu	Ala	Ala	Gly	Gln	Val	Leu	Ser	Gly	Val	Gly	Phe	Ser	Ile	130	135	140	
Pro	Ser	Gly	Leu	Val	Pro	Pro	Ser	Glu	Pro	Ser	Lys	Thr	Val	Ser	Ser	145	150	155	160
Thr	Thr	Glu	Glu	Leu	Gln	Asn	Glu	Ala	Gln	Ile	Arg	Glu	Ser	Ile	Val	165	170	175	
Lys	Thr	Phe	Phe	Pro	Thr	Phe	Glu	Arg	Gly	Val	Leu	Leu	Asn	Phe	Ser	180	185	190	
Glu	Leu	Phe	Lys	Pro	Lys	Pro	Val	Lys	Leu	Ala	Pro	Pro	Lys	Lys	Lys	195	200	205	
Thr	Pro	Lys	Val	Cys	Val	Pro	Gly	Arg	Leu	Thr	Leu	Glu	Val	Asp	Thr	210	215	220	
Asp	Tyr	Ala	Ile	Ile	Phe	Asn	Ser	Lys	Lys	Ser	Leu	Pro	Leu	Lys	Arg	225	230	235	240
Asn	Val	Val	Ser	Pro	Ile	Ser	Thr	His	Thr	Lys	Lys	Arg	Arg	Arg	Thr	245	250	255	
Ala	Asn	Thr	Ser	Gln	Arg	Asn	Asp	Gly	Leu	Asp	Leu	Asn	Thr	Val	Phe	260	265	270	
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Ile	Asp	Phe	Ala	Phe	Asp	Glu	Asn	Ile	Phe	Asp	Gly	Asp	Thr	Gly	Thr	305	310	315	320
Ser	Lys	Val	Val	Leu	Asn	Leu	Asn	Asp	Pro	Lys	Leu	Leu	Leu	Gln	Pro	325	330	335	
Gln	Leu	Pro	Lys	Glu	Asp	Ser	Gln	Arg	Ser	Phe	Ala	Asp	Thr	His		340	345	350	
Gln	Arg	Asn	Ser	Leu	Ala	Trp	Lys	Phe	Asn	Ile	Ser	Asn	Asp	Pro	Ala	355	360	365	
Tyr	Glu	Met	Leu	Lys	Gln	Asn	His	Gln	Ser	Lys	Val	Arg	Asn	Thr	Leu	370	375	380	
Ser	Gln	Leu	Ala	Ile	Glu	His	Ala	Ala	Phe	Ala	Glu	Lys	Leu	Thr	Phe	385	390	395	400
Pro	Tyr	Tyr	Lys	Thr	Arg	Leu	Ser	Lys	Arg	Ala	Val	Arg	Ser	Tyr	His	405	410	415	
Arg	Pro	Thr	Met	Ser	Phe	Lys	Pro	Asn	Ala	Ala	Ile	Val	Phe	Ser	Pro	420	425	430	
Leu	Ile	Val	Arg	Lys	Arg	Ser	Lys	Asp	Lys	His	Lys	Ser	Glu	Arg	Glu	435	440	445	

Leu	Ile	Pro	Thr	Thr	Lys	Glu	Ile	Thr	Met	Gly	Asp	Thr	Thr	His	Ala	
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Ile	Leu	Val	Glu	Phe	Ser	Glu	Glu	His	Pro	Ala	Val	Leu	Ser	Asn	Ala	
465					470					475					480	
Gly	Met	Ala	Ser	Arg	Ile	Val	Asn	Tyr	Tyr	Arg	Lys	Lys	Asn	Glu	Gln	
				485					490					495		
Asp	Glu	Ser	Arg	Pro	Lys	Leu	Glu	Val	Gly	Glu	Ser	His	Val	Leu	Asp	
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Val	Gln	Asp	Arg	Ser	Pro	Phe	Trp	Asn	Phe	Gly	Ser	Val	Glu	Pro	Gly	
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Val	Ala	Lys	Gln	Gln	Arg	Ala	Tyr	Glu	Glu	Glu	Ile	Asn	Arg	Ile	Trp	
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Asn	Ala	Gln	Lys	Arg	Gly	Leu	Ser	Ile	Asn	Asn	Leu	Glu	Glu	Leu	Ala	
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Glu	Thr	Ile	His	Asp	Pro	Ile	Val	Ile	His	Ala	Tyr	Leu	Lys	Lys	Arg	
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Arg	Glu	Ile	Asp	Glu	Gln	Ser	Thr	Ala	Leu	Asp	Ala	Val	Val	Pro	Thr	
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Gly	Asp	Glu	Ala	Ile	Asp	Arg	Arg	Asn	Arg	Arg	Arg	Leu	Glu	Gln	Glu	

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Leu	Ala	Lys	Ser	Gln	Lys	Asn	Trp	Glu	Arg	Arg	Arg	Ala	Arg	His	Ala		
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<400> 5

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Arg	Glu	Asp	Gly	Ala	Val	Lys	Ala	Gln	Asp	Asp	Ala	Ile	Asp	Tyr	Ser		
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Asp	Ile	Thr	Glu	Leu	Ser	Glu	Asp	Cys	Pro	Arg	Thr	Pro	Pro	Glu	Glu		
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Thr	Ser	Thr	Tyr	Asp	Asp	Leu	Glu	Asp	Ala	Ile	Pro	Ala	Ser	Lys	Val		
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Glu	Ala	Lys	Leu	Thr	Lys	Asp	Asp	Lys	Glu	Leu	Met	Pro	Pro	Pro	Ser		
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Ala	Pro	Met	Arg	Ser	Gly	Ser	Gly	Gly	Gly	Ile	Glu	Glu	Pro	Ala	Lys		
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Ser	Asn	Asp	Ala	Ser	Ser	Pro	Ser	Asp	Asp	Ser	Lys	Ser	Thr	Asp	Ser		
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Lys	Asp	Ala	Asp	Arg	Lys	Leu	Asp	Thr	Pro	Leu	Ala	Asp	Ile	Leu	Pro		
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Ser	Lys	Tyr	Gln	Asn	Val	Asp	Val	Arg	Glu	Leu	Phe	Pro	Asp	Phe	Arg		
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Pro	Gln	Lys	Val	Leu	Arg	Phe	Ser	Arg	Leu	Phe	Gly	Pro	Gly	Lys	Pro		
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Thr	Ser	Leu	Pro	Gln	Ile	Trp	Arg	His	Val	Arg	Lys	Arg	Arg	Arg	Lys		
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Ser	Pro	Ser	Asp	Thr	Glu	Glu	Pro	Arg	Lys	Arg	Gly	Phe	Ser	Leu	His		
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Tyr	Ala	Ala	Glu	Pro	Thr	Pro	Ala	Glu	Cys	Met	Ser	Asp	Asp	Glu	Asp		

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Phe	Gly	Pro	Ala	Gln	Ile	Trp	Tyr	Asp	Ile	Leu	Glu	Val	Pro	Asp
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Ser	Gln	Gln	Gln	Leu	Lys	Asp	Glu	Arg	Arg	Val	Lys	Ser	Pro	Glu
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Asp	Val	Glu	Asp	Pro	Ser	Ile	Ala	Asp	Asp	Ala	Phe	Leu	Met	Val
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Gln	Leu	His	Trp	Glu	Asp	Asp	Val	Val	Trp	Asp	Gly	Asn	Asp	Ile
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Ala	Lys	Val	Leu	Gln	Lys	Leu	Asn	Ser	Lys	Thr	Asn	Ala	Ala	Gly
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Leu	Pro	Ser	Ser	Gly	Ser	Arg	Thr	Ala	Gly	Ala	Phe	Ser	Gln	Pro
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Lys	Pro	Ser	Met	Pro	Val	Gly	Ser	Gly	Ser	Ser	Lys	Gln	Gly	Ser
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Ala	Ser	Ser	Lys	Lys	Ala	Gln	Gln	Asn	Ala	Gln	Ala	Lys	Pro	Ala
				485					490					495
Ala	Pro	Asp	Asp	Thr	Trp	Tyr	Ser	Leu	Phe	Pro	Val	Glu	Asn	Glu
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Leu	Ile	Tyr	Tyr	Lys	Trp	Glu	Asp	Glu	Val	Ile	Trp	Asp	Ala	Gln
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Val	Ser	Lys	Val	Pro	Lys	Pro	Lys	Val	Leu	Thr	Leu	Asp	Pro	Asn
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Glu	Asn	Ile	Ile	Leu	Gly	Ile	Pro	Asp	Asp	Ile	Asp	Pro	Ser	Lys
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Asn	Lys	Ser	Thr	Gly	Pro	Pro	Pro	Lys	Ile	Lys	Ile	Pro	His	Pro
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Val	Lys	Lys	Ser	Lys	Ile	Leu	Leu	Gly	Lys	Ala	Gly	Val	Ile	Asn
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Leu	Ala	Glu	Asp	Thr	Pro	Pro	Pro	Pro	Pro	Lys	Ser	Pro	Asp	Arg
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Pro	Phe	Asn	Ile	Ser	Asn	Asp	Thr	Tyr	Tyr	Thr	Pro	Lys	Thr	Glu
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Thr	Leu	Arg	Leu	Lys	Val	Gly	Gly	Asn	Leu	Ile	Gln	His	Ser	Thr
625					630					635				640
Val	Val	Glu	Leu	Arg	Ala	Pro	Phe	Val	Pro	Thr	His	Met	Gly	Pro
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Asn	Val	Arg	Ala	Phe	His	Arg	Pro	Pro	Leu	Lys	Lys	Tyr	Ser	His
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Pro	Met	Ala	Gln	Ser	Ile	Pro	His	Pro	Val	Phe	Pro	Leu	Leu	Lys
				675				680						685
Ile	Ala	Lys	Lys	Ala	Lys	Gln	Arg	Glu	Val	Glu	Arg	Ile	Ala	Ser
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Gly	Gly	Asp	Val	Phe	Phe	Met	Arg	Asn	Pro	Glu	Asp	Leu	Ser	Gly
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Asp	Gly	Asp	Ile	Val	Leu	Ala	Glu	Phe	Cys	Glu	Glu	His	Pro	Pro
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Ile	Asn	Gln	Val	Gly	Met	Cys	Ser	Lys	Ile	Lys	Asn	Tyr	Tyr	Lys
				740				745						750
Lys	Ala	Glu	Lys	Asp	Ser	Gly	Pro	Gln	Asp	Tyr	Val	Tyr	Gly	Glu
				755				760						765

Ala	Phe	Ala	His	Thr	Ser	Pro	Phe	Leu	Gly	Ile	Leu	His	Pro	Gly	Gln	770	775	780
Cys	Ile	Gln	Ala	Ile	Glu	Asn	Asn	Met	Tyr	Arg	Ala	Pro	Ile	Tyr	Pro	785	790	795
His	Lys	Met	Ala	His	Asn	Asp	Phe	Leu	Val	Ile	Arg	Thr	Arg	Asn	Asn	805	810	815
Tyr	Trp	Ile	Arg	Ser	Val	Asn	Ser	Ile	Tyr	Thr	Val	Gly	Gln	Glu	Cys	820	825	830
Pro	Leu	Tyr	Glu	Val	Pro	Gly	Pro	Asn	Ser	Lys	Arg	Ala	Asn	Asn	Phe	835	840	845
Thr	Arg	Asp	Phe	Leu	Gln	Val	Phe	Ile	Tyr	Arg	Leu	Phe	Trp	Lys	Ser	850	855	860
Arg	Asp	Asn	Pro	Arg	Arg	Ile	Arg	Met	Asp	Asp	Ile	Lys	Gln	Ala	Phe	865	870	875
Pro	Ala	His	Ser	Glu	Ser	Ser	Ile	Arg	Lys	Arg	Leu	Lys	Gln	Cys	Ala	885	890	895
Asp	Phe	Lys	Arg	Thr	Gly	Met	Asp	Ser	Asn	Trp	Trp	Val	Ile	Lys	Pro	900	905	910
Glu	Phe	Arg	Leu	Pro	Ser	Glu	Glu	Glu	Ile	Arg	Ala	Met	Val	Ser	Pro	915	920	925
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Lys	Asp	Ala	Gly	Tyr	Gly	Glu	Lys	Phe	Leu	Phe	Ala	Pro	Gln	Glu	Asp	945	950	955
Asp	Asp	Glu	Glu	Ala	Gln	Leu	Lys	Leu	Asp	Asp	Glu	Val	Lys	Val	Ala	965	970	975
Pro	Trp	Asn	Thr	Arg	Ala	Tyr	Ile	Gln	Ala	Met	Arg	Gly	Lys	Cys		980	985	990
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Phe	Ser	Tyr	Val	Arg	Val	Pro	Asn	Lys	Pro	Thr	Gln	Thr	Lys	Glu	Glu	1010	1015	1020
Gln	Glu	Ser	Gln	Pro	Lys	Arg	Ser	Val	Thr	Gly	Thr	Asp	Ala	Asp	Leu	1025	1030	1035
Arg	Arg	Leu	Pro	Leu	Gln	Arg	Ala	Lys	Glu	Leu	Leu	Arg	Gln	Phe	Lys	1045	1050	1055
Val	Pro	Glu	Glu	Glu	Ile	Lys	Lys	Leu	Ser	Arg	Trp	Glu	Val	Ile	Asp	1060	1065	1070
Val	Val	Arg	Thr	Leu	Ser	Thr	Glu	Lys	Ala	Lys	Ala	Gly	Glu	Glu	Gly	1075	1080	1085
Met	Asp	Lys	Phe	Ser	Arg	Gly	Asn	Arg	Phe	Ser	Ile	Ala	Glu	His	Gln	1090	1095	1100
Glu	Arg	Tyr	Lys	Glu	Glu	Cys	Gln	Arg	Ile	Phe	Asp	Leu	Gln	Asn	Arg	1105	1110	1115
Val	Leu	Ala	Ser	Ser	Glu	Val	Leu	Ser	Thr	Asp	Glu	Ala	Glu	Ser	Ser	1125	1130	1135
Ala	Ser	Glu	Glu	Ser	Asp	Leu	Glu	Glu	Leu	Gly	Lys	Asn	Leu	Glu	Asn	1140	1145	1150
Met	Leu	Ser	Asn	Lys	Lys	Thr	Ser	Thr	Gln	Leu	Ser	Arg	Glu	Arg	Glu	1155	1160	1165
Glu	Leu	Glu	Arg	Gln	Glu	Leu	Leu	Arg	Gln	Leu	Asp	Glu	Glu	His	Gly	1170	1175	1180
Gly	Pro	Ser	Gly	Ser	Gly	Gly	Ala	Lys	Gly	Ala	Lys	Gly	Lys	Asp	Asp	1185	1190	1195
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 Phe Ser Glu His Cys Gly Gln Leu Glu Asn Asn Ile Ala Lys Thr Gln
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 Gln Cys Ser Thr Asp Asp Glu Asp Asp Asp Glu Glu Glu Asp Phe Gln
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 Glu Val Ser Glu Asp Glu Asn Asn Ala Ala Ser Ile Leu Asp Gln Gly
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 Glu Arg Ile Asn Ala Pro Ala Asp Ala Met Asp Gly Met Phe Asp Pro
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 Lys Asn Ile Lys Thr Glu Ile Asp Leu Glu Ala His Gln Met Ala Asp
 1860 1865 1870
 Glu Ser Met Asp Val Asp Pro Asn Tyr Asp Pro Ser Asp Phe Leu Ala
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 Met His Lys Gln Arg Gln Ser Leu Gly Glu Pro Ser Ser Leu Gln Gly
 1890 1895 1900
 Ala Phe Thr Asn Phe Leu Ser His Glu Gln Asp Asp Asn Gly Pro Tyr
 1905 1910 1915 1920
 Asn Pro Ala Glu Ala Ser Thr Ser Ala Ala Ser Gly Ala Asp Leu Gly
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 Met Asp Ala Ser Met Ala Met Gln Met Ala Pro Glu Met Pro Val Asn
 1940 1945 1950
 Thr Met Asn Asn Gly Met Gly Ile Asp Asp Asp Leu Asp Ile Ser Glu
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 Ser Asp Glu Glu Asp Asp Gly Ser Arg Val Arg Ile Lys Lys Glu Val
 1970 1975 1980
 Phe Asp Asp Gly Asp Tyr Ala Leu Gln His Gln Gln Met Gly Gln Ala
 1985 1990 1995 2000
 Ala Ser Gln Ser Gln Ile Tyr Met Val Asp Ser Ser Asn Glu Pro Thr
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Leu	Thr	Ala	Asn	Glu	Glu	Leu	Thr	Gly	Thr	Asp	Gly	Ala	Leu	Val	Asn
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Asp	Glu	Gly	Trp	Val	Arg	Ser	Thr	Glu	Asp	Ala	Val	Asp	Tyr	Ser	Asp
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Pro	Pro	Pro	Gly	Pro	Met	Lys	Lys	Asp	Lys	Asp	Gln	Asp	Ser	Ile	Thr
				165					170					175	
Gly	Glu	Lys	Val	Asp	Phe	Ser	Ser	Ser	Ser	Asp	Ser	Glu	Ser	Glu	Met
			180					185					190		
Gly	Pro	Gln	Glu	Ala	Thr	Gln	Ala	Glu	Ser	Glu	Asp	Gly	Lys	Leu	Thr
		195					200					205			
Leu	Pro	Leu	Ala	Gly	Ile	Met	Gln	His	Asp	Ala	Thr	Lys	Leu	Leu	Pro
		210				215					220				
Ser	Val	Thr	Glu	Leu	Phe	Pro	Glu	Phe	Arg	Pro	Gly	Lys	Val	Leu	Arg
225					230					235					240
Phe	Leu	Arg	Leu	Phe	Gly	Pro	Gly	Lys	Asn	Val	Pro	Ser	Val	Trp	Arg
			245						250					255	
Ser	Ala	Arg	Arg	Lys	Arg	Lys	Lys	Lys	His	Arg	Glu	Leu	Ile	Gln	Glu
			260					265					270		
Glu	Gln	Ile	Gln	Glu	Val	Glu	Cys	Ser	Val	Glu	Ser	Glu	Val	Ser	Gln
		275					280					285			
Lys	Ser	Leu	Trp	Asn	Tyr	Asp	Tyr	Ala	Pro	Pro	Pro	Pro	Pro	Glu	Gln
		290				295					300				
Cys	Leu	Ser	Asp	Asp	Glu	Ile	Thr	Met	Met	Ala	Pro	Val	Glu	Ser	Lys
305					310					315					320
Phe	Ser	Gln	Ser	Thr	Gly	Asp	Ile	Asp	Lys	Val	Thr	Asp	Thr	Lys	Pro
			325						330					335	
Arg	Val	Ala	Glu	Trp	Arg	Tyr	Gly	Pro	Ala	Arg	Leu	Trp	Tyr	Asp	Met
			340					345					350		
Leu	Gly	Val	Pro	Glu	Asp	Gly	Ser	Gly	Phe	Asp	Tyr	Gly	Phe	Lys	Leu
		355					360					365			
Arg	Lys	Thr	Glu	His	Glu	Pro	Val	Ile	Lys	Ser	Arg	Met	Ile	Glu	Glu
		370				375					380				
Phe	Arg	Lys	Leu	Glu	Glu	Asn	Asn	Gly	Thr	Asp	Leu	Leu	Ala	Asp	Glu
385					390					395					400
Asn	Phe	Leu	Met	Val	Thr	Gln	Leu	His	Trp	Glu	Asp	Asp	Ile	Ile	Trp
			405						410					415	
Asp	Gly	Glu	Asp	Val	Lys	His	Lys	Gly	Thr	Lys	Pro	Gln	Arg	Ala	Ser
			420					425				430			
Leu	Ala	Gly	Trp	Leu	Pro	Ser	Ser	Met	Thr	Arg	Asn	Ala	Met	Ala	Tyr
		435					440					445			
Asn	Val	Gln	Gln	Gly	Phe	Ala	Ala	Thr	Leu	Asp	Asp	Asp	Lys	Pro	Trp

450					455					460					
Tyr 465	Ser	Ile	Phe	Pro	Ile 470	Asp	Asn	Glu	Asp	Leu 475	Val	Tyr	Gly	Arg	Trp 480
Glu	Asp	Asn	Ile	Ile 485	Trp	Asp	Ala	Gln	Ala 490	Met	Pro	Arg	Leu	Leu	Glu 495
Pro	Pro	Val	Leu	Thr 500	Leu	Asp	Pro	Asn	Asp 505	Glu	Asn	Leu	Ile	Leu	Glu 510
Ile	Pro	Asp	Glu	Lys 515	Glu	Glu	Ala	Thr	Ser 520	Asn	Ser	Pro	Ser	Lys	Glu 525
Ser	Lys 530	Lys	Glu	Ser	Ser	Leu 535	Lys	Lys	Ser	Arg	Ile 540	Leu	Leu	Gly	Lys 545
Thr 545	Gly	Val	Ile	Lys	Glu 550	Glu	Pro	Gln	Gln	Asn 555	Met	Ser	Gln	Pro	Glu 560
Val	Lys	Asp	Pro	Trp 565	Asn	Leu	Ser	Asn	Asp 570	Glu	Tyr	Tyr	Tyr	Pro	Lys 575
Gln	Gln	Gly	Leu	Arg 580	Gly	Thr	Phe	Gly	Gly 585	Asn	Ile	Ile	Gln	His	Ser 590
Ile	Pro	Ala 595	Val	Glu	Leu	Arg	Gln	Pro	Phe	Phe	Pro	Thr 605	His	Met	Gly 610
Pro	Ile 610	Lys	Leu	Arg	Gln	Phe 615	His	Arg	Pro	Pro	Leu 620	Lys	Lys	Tyr	Ser 625
Phe 625	Gly	Ala	Leu	Ser	Gln	Pro 630	Gly	Pro	His	Ser	Val	Gln	Pro	Leu	Leu 640
Lys	His	Ile	Lys	Lys 645	Lys	Ala	Lys	Met	Arg	Glu 650	Gln	Glu	Arg	Gln	Ala 655
Ser	Gly	Gly	Gly 660	Glu	Met	Phe	Phe	Met	Arg 665	Thr	Pro	Gln	Asp	Leu	Thr 670
Gly	Lys	Asp 675	Gly	Asp	Leu	Ile	Leu 680	Ala	Glu	Tyr	Ser	Glu 685	Glu	Asn	Gly 690
Pro	Leu 690	Met	Met	Gln	Val	Gly 695	Met	Ala	Thr	Lys	Ile 700	Lys	Asn	Tyr	Tyr 705
Lys 705	Arg	Lys	Pro	Gly	Lys 710	Asp	Pro	Gly	Ala	Pro 715	Asp	Cys	Lys	Tyr	Gly 720
Glu	Thr	Val	Tyr	Cys 725	His	Thr	Ser	Pro	Phe	Leu 730	Gly	Ser	Leu	His	Pro 735
Gly	Gln	Leu	Leu 740	Gln	Ala	Phe	Glu	Asn	Asn 745	Leu	Phe	Arg	Ala	Pro	Ile 750
Tyr	Leu 755	His	Lys	Met	Pro	Glu	Thr 760	Asp	Phe	Leu	Ile	Ile 765	Arg	Thr	Arg 770
Gln	Gly 770	Tyr	Tyr	Ile	Arg	Glu	Leu 775	Val	Asp	Ile	Phe	Val 780	Val	Gly	Gln 785
Gln 785	Cys	Pro	Leu	Phe	Glu 790	Val	Pro	Gly	Pro	Asn 795	Ser	Lys	Arg	Ala	Asn 800
Thr	His	Ile	Arg	Asp 805	Phe	Leu	Gln	Val	Phe	Ile 810	Tyr	Arg	Leu	Phe	Trp 815
Lys	Ser	Lys	Asp 820	Arg	Pro	Arg	Arg	Ile	Arg 825	Met	Glu	Asp	Ile	Lys	Lys 830
Ala	Phe	Pro	Ser 835	His	Ser	Glu	Ser	Ser	Ile 840	Arg	Lys	Arg	Leu	Lys	Leu 845
Cys	Ala	Asp	Phe 850	Lys	Arg	Thr	Gly	Met	Asp 855	Ser	Asn	Trp	Trp	Val	Leu 860
Lys 865	Ser	Asp	Phe	Arg	Leu 870	Pro	Thr	Glu	Glu	Glu 875	Ile	Arg	Ala	Met	Val 880
Ser	Pro	Glu	Gln	Cys 885	Cys	Ala	Tyr	Tyr	Ser 890	Met	Ile	Ala	Ala	Glu	Gln 895
Arg	Leu	Lys	Asp 900	Ala	Gly	Tyr	Gly	Glu	Lys 905	Ser	Phe	Phe	Ala	Pro	Glu 910

Glu Glu Asn Glu Glu Asp Phe Gln Met Lys Ile Asp Asp Glu Val Arg
 915 920 925
 Thr Ala Pro Trp Asn Thr Thr Arg Ala Phe Ile Ala Ala Met Lys Gly
 930 935 940
 Lys Cys Leu Leu Glu Val Thr Gly Val Ala Asp Pro Thr Gly Cys Gly
 945 950 955 960
 Glu Gly Phe Ser Tyr Val Lys Ile Pro Asn Lys Pro Thr Gln Gln Lys
 965 970 975
 Asp Asp Lys Glu Pro Gln Pro Val Lys Lys Thr Val Thr Gly Thr Asp
 980 985 990
 Ala Asp Leu Arg Arg Leu Ser Leu Lys Asn Ala Lys Gln Leu Leu Arg
 995 1000 1005
 Lys Phe Gly Val Pro Glu Glu Glu Ile Lys Lys Leu Ser Arg Trp Glu
 1010 1015 1020
 Val Ile Asp Val Val Arg Thr Met Ser Thr Glu Gln Ala Arg Ser Gly
 1025 1030 1035 1040
 Glu Gly Pro Met Ser Lys Phe Ala Arg Gly Ser Arg Phe Ser Val Ala
 1045 1050 1055
 Glu His Gln Glu Arg Tyr Lys Glu Glu Cys Gln Arg Ile Phe Asp Leu
 1060 1065 1070
 Gln Asn Lys Val Leu Ser Ser Thr Glu Val Leu Ser Thr Asp Thr Asp
 1075 1080 1085
 Ser Ser Ser Ala Glu Asp Ser Asp Phe Glu Glu Met Gly Lys Asn Ile
 1090 1095 1100
 Glu Asn Met Leu Gln Asn Lys Lys Thr Ser Ser Gln Leu Ser Arg Glu
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 Arg Glu Glu Gln Glu Arg Lys Glu Leu Gln Arg Met Leu Leu Ala Ala
 1125 1130 1135
 Gly Ser Ala Ala Ser Gly Asn Asn His Arg Asp Asp Asp Thr Ala Ser
 1140 1145 1150
 Val Thr Ser Leu Asn Ser Ser Ala Thr Gly Arg Cys Leu Lys Ile Tyr
 1155 1160 1165
 Arg Thr Phe Arg Asp Glu Glu Gly Lys Glu Tyr Val Arg Cys Glu Thr
 1170 1175 1180
 Val Arg Lys Pro Ala Val Ile Asp Ala Tyr Val Arg Ile Arg Thr Thr
 1185 1190 1195 1200
 Lys Asp Glu Glu Phe Ile Arg Lys Phe Ala Leu Phe Asp Glu Gln His
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 Arg Glu Glu Met Arg Lys Glu Arg Arg Arg Ile Gln Glu Gln Leu Arg
 1220 1225 1230
 Arg Leu Lys Arg Asn Gln Glu Lys Glu Lys Leu Lys Gly Pro Pro Glu
 1235 1240 1245
 Lys Lys Pro Lys Lys Met Lys Glu Arg Pro Asp Leu Lys Leu Lys Cys
 1250 1255 1260
 Gly Ala Cys Gly Ala Ile Gly His Met Arg Thr Asn Lys Phe Cys Pro
 1265 1270 1275 1280
 Leu Tyr Tyr Gln Thr Asn Ala Pro Pro Ser Asn Pro Val Ala Met Thr
 1285 1290 1295
 Glu Glu Gln Glu Glu Leu Glu Lys Thr Val Ile His Asn Asp Asn
 1300 1305 1310
 Glu Glu Leu Ile Lys Val Glu Gly Thr Lys Ile Val Leu Gly Lys Gln
 1315 1320 1325
 Leu Ile Glu Ser Ala Asp Glu Val Arg Arg Lys Ser Leu Val Leu Lys
 1330 1335 1340
 Phe Pro Lys Gln Gln Leu Pro Pro Lys Lys Lys Arg Arg Val Gly Thr
 1345 1350 1355 1360
 Thr Val His Cys Asp Tyr Leu Asn Arg Pro His Lys Ser Ile His Arg

[illegible]

Val Ser Glu Glu Glu Glu Asp Glu Glu Glu Glu Glu Gln Arg Ser Gly
 1825 1830 1835 1840
 Pro Ser Val Leu Ser Gln Val His Leu Ser Glu Asp Glu Glu Asp Ser
 1845 1850 1855
 Glu Asp Phe His Ser Ile Ala Gly Asp Ser Asp Leu Asp Ser Asp Glu
 1860 1865 1870

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 <212> PRT
 <213> C. albicans

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 Asn Val Gln Asp Glu Glu Glu Asp Asp Asp Ile Phe Asn Gly Gln Ile
 35 40 45
 Asn Leu Asp Lys Leu Lys Leu Asp Met Asn Asp Pro Asn Leu Leu Phe
 50 55 60
 Val Pro Ser Lys Lys Val Asp Ala Thr Lys Ser Val Val Pro Ser Thr
 65 70 75 80
 Asp Lys Leu Leu Glu Leu Lys Phe Asn Ile Ser Asn Asp Gln Glu Tyr
 85 90 95
 Glu Leu Leu Arg Lys Asn Tyr Asn Thr Lys Gln Arg Ser Gln Leu Ser
 100 105 110
 Asn Leu Asn Ile Glu His Ser Val Pro Ala Leu Arg Leu Gln Thr Pro
 115 120 125
 Tyr Tyr Lys Val Lys Leu Ser Thr Asp Glu Thr Arg Ser Phe His Arg
 130 135 140
 Pro Val Phe Asn Val Arg Pro Gly Thr Leu Val Ser Phe Ser Lys Leu
 145 150 155 160
 Lys Leu Arg Lys Arg Lys Lys Asp Lys Gly Lys Ser Leu Gln Gln Ile
 165 170 175
 Phe Ser Lys Thr Ser Asp Leu Thr Val Ala Asp Thr Gly Asn Ile Ile
 180 185 190
 Ala Leu Glu Tyr Ser Glu Gln Tyr Pro Pro Ile Leu Ser Asn Phe Gly
 195 200 205
 Met Gly Ser Lys Leu Ile Asn Tyr Tyr Arg Lys Glu Arg Pro Asn Asp
 210 215 220
 Thr Ser Arg Pro Lys Ala Gln Ile Gly Glu Thr His Ile Leu Gly Val
 225 230 235 240
 Glu Asp Arg Ser Pro Phe Trp Asn Phe Gly Glu Val Ala Pro Gly Asp
 245 250 255
 Phe Val Pro Thr Leu Tyr Asn Asn Met Val Arg Ala Pro Ile Phe Lys
 260 265 270
 His Asp Asn Lys Pro Thr Asp Phe Leu Leu Val Lys Ser Gln Gly Ala
 275 280 285
 Gly Ser His Gln Lys Phe Tyr Leu Arg Gly Ile Asn Phe Asn Phe Ala
 290 295 300
 Val Gly Asn Thr Phe Pro Val Glu Val Pro Ala Pro His Ser Arg Lys
 305 310 315 320
 Val Thr Asn Ile Ser Lys Asn Arg Leu Lys Met Val Val Phe Arg Val
 325 330 335
 Met Asn Ser Leu Gly Val Pro Arg Ile Ser Val Lys Asp Val Ser Lys
 340 345 350

His	Phe	Pro	Glu	His	Ser	Asp	Met	Gln	Asn	Arg	Gln	Arg	Leu	Lys	Glu
		355					360					365			
Phe	Met	Glu	Tyr	Gln	Arg	Gln	Gly	Glu	Asp	Gln	Gly	Tyr	Trp	Lys	Val
	370					375				380					
Arg	Gly	Leu	Asn	Asp	Val	Ile	Pro	Gly	Glu	Glu	Glu	Ile	Arg	Thr	Met
385				390					395						400
Ile	Thr	Pro	Glu	Asp	Ser	Ser	Leu	Met	Asp	Thr	Met	Gln	Phe	Gly	Gln
			405					410						415	
Gln	Val	Leu	Asp	Asp	Asn	Met	Val	Leu	Phe	Gly	Glu	Gln			
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<212> PRT

<213> S. cerevisiae

<400> 8

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		20						25					30		
Asp	Ala	Lys	Leu	Lys	Glu	Ser	Lys	His	Ala	Glu	Leu	Asn	Met	Asn	Asp
	35					40						45			
Glu	Lys	Leu	Leu	Leu	Met	Ile	Glu	Lys	Thr	Asn	Asn	Leu	Ala	Gln	Gln
	50				55						60				
Lys	Gln	Gln	Leu	Asp	Ser	Ser	Asn	Leu	Ile	Leu	Pro	Leu	Asn	Glu	Thr
65				70					75					80	
Ile	Leu	Gln	Gln	Lys	Phe	Asn	Leu	Ser	Asn	Asp	Asp	Lys	Tyr	Gln	Ile
			85					90						95	
Leu	Lys	Lys	Thr	His	Gln	Thr	Lys	Val	Arg	Ser	Thr	Ile	Ser	Asn	Leu
		100						105					110		
Asn	Ile	Gln	His	Ser	Gln	Pro	Ala	Ile	Asn	Leu	Gln	Ser	Pro	Phe	Tyr
	115						120					125			
Lys	Val	Ala	Val	Pro	Arg	Tyr	Gln	Leu	Arg	His	Phe	His	Arg	Glu	Asn
	130					135					140				
Phe	Gly	Ser	His	Ile	Arg	Pro	Gly	Thr	Lys	Ile	Val	Phe	Ser	Lys	Leu
145				150					155					160	
Lys	Ala	Arg	Lys	Arg	Lys	Arg	Asp	Lys	Gly	Lys	Asp	Val	Lys	Glu	Ser
			165					170						175	
Phe	Ser	Thr	Ser	Gln	Asp	Leu	Thr	Ile	Gly	Asp	Thr	Ala	Pro	Val	Tyr
		180					185						190		
Leu	Met	Glu	Tyr	Ser	Glu	Gln	Thr	Pro	Val	Ala	Leu	Ser	Lys	Phe	Gly
	195						200					205			
Met	Ala	Asn	Lys	Leu	Ile	Asn	Tyr	Tyr	Arg	Lys	Ala	Asn	Glu	Gln	Asp
	210				215						220				
Thr	Leu	Arg	Pro	Lys	Leu	Pro	Val	Gly	Glu	Thr	His	Val	Leu	Gly	Val
225				230					235					240	
Gln	Asp	Lys	Ser	Pro	Phe	Trp	Asn	Phe	Gly	Phe	Val	Glu	Pro	Gly	His
			245					250						255	
Ile	Val	Pro	Thr	Leu	Tyr	Asn	Asn	Met	Ile	Arg	Ala	Pro	Val	Phe	Lys
		260					265					270			
His	Asp	Ile	Ser	Gly	Thr	Asp	Phe	Leu	Leu	Thr	Lys	Ser	Ser	Gly	Phe
	275					280						285			
Gly	Ile	Ser	Asn	Arg	Phe	Tyr	Leu	Arg	Asn	Ile	Asn	His	Leu	Phe	Thr
	290				295					300					
Val	Gly	Gln	Thr	Phe	Pro	Val	Glu	Glu	Ile	Pro	Gly	Pro	Asn	Ser	Arg
305					310					315					320

Lys Val Thr Ser Met Lys Ala Thr Arg Leu Lys Met Ile Ile Tyr Arg
 325 330 335
 Ile Leu Asn His Asn His Ser Lys Ala Ile Ser Ile Asp Pro Ile Ala
 340 345 350
 Lys His Phe Pro Asp Gln Asp Tyr Gly Gln Asn Arg Gln Lys Val Lys
 355 360 365
 Glu Phe Met Lys Tyr Gln Arg Asp Gly Pro Glu Lys Gly Leu Trp Arg
 370 375 380
 Leu Lys Asp Asp Glu Lys Leu Leu Asp Asn Glu Ala Val Lys Ser Leu
 385 390 395 400
 Ile Thr Pro Glu Gln Ile Ser Gln Val Glu Ser Met Ser Gln Gly Leu
 405 410 415
 Gln Phe Gln Glu Asp Asn Glu Ala Tyr Asn Phe Asp Ser Lys Leu Lys
 420 425 430
 Ser Leu

<210> 9
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 <212> PRT
 <213> S. pombe

<400> 9
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 Thr Ser Lys Val Val Leu Asn Leu Asn Asp Pro Lys Leu Leu Gln
 35 40 45
 Pro Gln Leu Pro Lys Lys Glu Asp Ser Gln Arg Ser Phe Ala Asp Thr
 50 55 60
 His Gln Arg Asn Ser Leu Ala Trp Lys Phe Asn Ile Ser Asn Asp Pro
 65 70 75 80
 Ala Tyr Glu Met Leu Lys Gln Asn His Gln Ser Lys Val Arg Asn Thr
 85 90 95
 Leu Ser Gln Leu Ala Ile Glu His Ala Ala Phe Ala Glu Lys Leu Thr
 100 105 110
 Phe Pro Tyr Tyr Lys Thr Arg Leu Ser Lys Arg Ala Val Arg Ser Tyr
 115 120 125
 His Arg Pro Thr Met Ser Phe Lys Pro Asn Ala Ala Ile Val Phe Ser
 130 135 140
 Pro Leu Ile Val Arg Lys Arg Ser Lys Asp Lys His Lys Ser Glu Arg
 145 150 155 160
 Glu Leu Ile Pro Thr Lys Glu Ile Thr Met Gly Asp Thr Thr His
 165 170 175
 Ala Ile Leu Val Glu Phe Ser Glu Glu His Pro Ala Val Leu Ser Asn
 180 185 190
 Ala Gly Met Ala Ser Arg Ile Val Asn Tyr Tyr Arg Lys Lys Asn Glu
 195 200 205
 Gln Asp Glu Ser Arg Pro Lys Leu Glu Val Gly Glu Ser His Val Leu
 210 215 220
 Asp Val Gln Asp Arg Ser Pro Phe Trp Asn Phe Gly Ser Val Glu Pro
 225 230 235 240
 Gly Glu Ile Thr Pro Thr Leu Tyr Asn Lys Met Ile Arg Ala Pro Leu
 245 250 255
 Phe Lys His Glu Val Pro Pro Thr Asp Phe Ile Leu Ile Arg Asn Ser
 260 265 270

Ser	Ser	Tyr	Gly	Ser	Lys	Tyr	Tyr	Leu	Lys	Asn	Ile	Asn	His	Met	Phe
		275					280					285			
Val	Ser	Gly	Gln	Thr	Phe	Pro	Val	Thr	Asp	Val	Pro	Gly	Pro	His	Ser
		290				295					300				
Arg	Lys	Val	Thr	Thr	Ala	Ser	Lys	Asn	Arg	Leu	Lys	Met	Leu	Val	Phe
305					310					315					320
Arg	Leu	Ile	Arg	Arg	Ser	Pro	Asn	Gly	Gly	Leu	Phe	Ile	Arg	Gln	Leu
				325					330					335	
Ser	Lys	His	Phe	Ser	Asp	Gln	Asn	Glu	Met	Gln	Ile	Arg	Gln	Arg	Leu
			340					345					350		
Lys	Glu	Phe	Met	Glu	Tyr	Lys	Lys	Gly	Asp	Gly	Pro	Gly	Tyr	Trp	
		355					360				365				
Lys	Leu	Lys	Ser	Asn	Glu	Val	Val	Pro	Asp	Glu	Ala	Gly	Thr	Arg	Ser
		370				375					380				
Met	Val	Ser	Pro	Glu	Thr	Val	Cys	Leu	Leu	Glu	Ser	Met	Gln	Val	Gly
385					390					395					400
Val	Arg	Gln	Leu	Glu	Asp	Ala	Gly	Tyr	Gly	Lys	Thr	Met	Asp	Glu	
			405						410					415	

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 <212> PRT
 <213> Homo sapiens

<400> 10

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Tyr	Asn	Val	Gln	Gly	Phe	Ala	Ala	Thr	Leu	Asp	Asp	Asp	Lys	Pro	
			20				25					30			
Trp	Tyr	Ser	Ile	Phe	Pro	Ile	Asp	Asn	Glu	Asp	Leu	Val	Tyr	Gly	Arg
		35					40					45			
Trp	Glu	Asp	Asn	Ile	Ile	Trp	Asp	Ala	Gln	Ala	Met	Pro	Arg	Leu	Leu
	50					55					60				
Glu	Pro	Pro	Val	Leu	Thr	Leu	Asp	Pro	Asn	Asp	Glu	Asn	Leu	Ile	Leu
65					70					75					80
Glu	Ile	Pro	Asp	Glu	Lys	Glu	Glu	Ala	Thr	Ser	Asn	Ser	Pro	Ser	Lys
				85					90					95	
Glu	Ser	Lys	Lys	Glu	Ser	Ser	Leu	Lys	Lys	Ser	Arg	Ile	Leu	Leu	Gly
			100					105					110		
Lys	Thr	Gly	Val	Ile	Lys	Glu	Glu	Pro	Gln	Gln	Asn	Met	Ser	Gln	Pro
		115					120					125			
Glu	Val	Lys	Asp	Pro	Trp	Asn	Leu	Ser	Asn	Asp	Glu	Tyr	Tyr	Tyr	Pro
	130					135					140				
Lys	Gln	Gln	Gly	Leu	Arg	Gly	Thr	Phe	Gly	Gly	Asn	Ile	Ile	Gln	His
145					150					155					160
Ser	Ile	Pro	Ala	Val	Glu	Leu	Arg	Gln	Pro	Phe	Phe	Pro	Thr	His	Met
			165						170					175	
Gly	Pro	Ile	Lys	Leu	Arg	Gln	Phe	His	Arg	Pro	Pro	Leu	Lys	Lys	Tyr
			180					185					190		
Ser	Phe	Gly	Ala	Leu	Ser	Gln	Pro	Gly	Pro	His	Ser	Val	Gln	Pro	Leu
		195					200					205			
Leu	Lys	His	Ile	Lys	Lys	Lys	Ala	Lys	Met	Arg	Glu	Gln	Glu	Arg	Gln
	210					215					220				
Ala	Ser	Gly	Gly	Gly	Glu	Met	Phe	Phe	Met	Arg	Thr	Pro	Gln	Asp	Leu
225					230					235					240
Thr	Gly	Lys	Asp	Gly	Asp	Leu	Ile	Leu	Ala	Glu	Tyr	Ser	Glu	Glu	Asn
				245					250					255	

Gly	Pro	Leu	Met	Met	Gln	Val	Gly	Met	Ala	Thr	Lys	Ile	Lys	Asn	Tyr
			260					265					270		
Tyr	Lys	Arg	Lys	Pro	Gly	Lys	Asp	Pro	Gly	Ala	Pro	Asp	Cys	Lys	Tyr
		275					280					285			
Gly	Glu	Thr	Val	Tyr	Cys	His	Thr	Ser	Pro	Phe	Leu	Gly	Ser	Leu	His
	290				295						300				
Pro	Gly	Gln	Leu	Leu	Gln	Ala	Phe	Glu	Asn	Asn	Leu	Phe	Arg	Ala	Pro
305					310				315						320
Ile	Tyr	Leu	His	Lys	Met	Pro	Glu	Thr	Asp	Phe	Leu	Ile	Ile	Arg	Thr
			325						330					335	
Arg	Gln	Gly	Tyr	Tyr	Ile	Arg	Glu	Leu	Val	Asp	Ile	Phe	Val	Val	Gly
		340					345						350		
Gln	Gln	Cys	Pro	Leu	Phe	Glu	Val	Pro	Gly	Pro	Asn	Ser	Lys	Arg	Ala
		355					360					365			
Asn	Thr	His	Ile	Arg	Asp	Phe	Leu	Gln	Val	Phe	Ile	Tyr	Arg	Leu	Phe
	370					375					380				
Trp	Lys	Ser	Lys	Asp	Arg	Pro	Arg	Arg	Ile	Arg	Met	Glu	Asp	Ile	Lys
385					390					395					400
Lys	Ala	Phe	Pro	Ser	His	Ser	Glu	Ser	Ser	Ile	Arg	Lys	Arg	Leu	Lys
			405						410					415	
Leu	Cys	Ala	Asp	Phe	Lys	Arg	Thr	Gly	Met	Asp	Ser	Asn	Trp	Trp	Val
		420						425					430		
Leu	Lys	Ser	Asp	Phe	Arg	Leu	Pro	Thr	Glu	Glu	Glu	Ile	Arg	Ala	Met
	435						440					445			
Val	Ser	Pro	Glu	Gln	Cys	Cys	Ala	Tyr	Tyr	Ser	Met	Ile	Ala	Ala	Glu
	450				455						460				
Gln	Arg	Leu	Lys	Asp	Ala	Gly	Tyr	Gly	Glu	Lys	Ser	Phe	Phe	Ala	Pro
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Glu															

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 35 40 45
 Lys Lys Ser Lys Glu Gln Asp Thr Glu Ile Asp Val Glu Glu Glu Leu
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 Ala Pro Trp Asn Leu Ser Arg Asn Phe Val
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> sequence source: Degenerate oligonucleotide designed and used to amplify fragments of DNA from Candida albicans strain SC5314 genomic DNA by polymerase chain reaction. n is defined as

Inosine.

<220>
<221> misc_feature
<222> (15)..(15)
<223> where n is inosine

<400> 12
ccwggwccwa aytcnadd 18

<210> 13
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> sequence source: Degenerate oligonucleotide designed and used to amplify fragments of DNA from Candida albicans strain SC5314 genomic DNA by polymerase chain reaction.

<400> 13
gayccwachg gwtgtggwa agg 23

<210> 14
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> sequence source: Degenerate oligonucleotide designed and used to amplify fragments of DNA from Candida albicans strain SC5314 genomic DNA by polymerase chain reaction.

<400> 14
cctttcwcca cawccagtwg grtc 24

<210> 15
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> sequence source: Degenerate oligonucleotide designed and used to amplify fragments of DNA from Candida albicans strain SC5314 genomic DNA by polymerase chain reaction. n is defined as Inosine.

<220>
<221> misc_feature
<222> (12)..(12)
<223> where n is inosine

<400> 15
ttrtttcayc tnartgwc 19

<210> 16
<211> 30

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> *S. cerevisiae* oligonucleotide

 <400> 16
 ccgctcgaga tgacacccaa cttaaagttc 30

 <210> 17
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> *S. cerevisiae* oligonucleotide

 <400> 17
 cgcgcatcca gagatttttag cttagaatc 29

 <210> 18
 <211> 37
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> *C. albicans* oligonucleotide

 <400> 18
 ggaattccat atgcttttgc tcaacaatcc cttggac 37

 <210> 19
 <211> 32
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> *C. albicans* oligonucleotide

 <400> 19
 cgcggatccc tgctctgctc accgaataac ac 32

 <210> 20
 <211> 37
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> *Homo sapiens* oligonucleotide

 <400> 20
 ggaattccat atgagcctgg caggctggct tccttct 37

 <210> 21
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Homo sapiens oligonucleotide

<400> 21

ccgctcgagt tctggagcaa aaaaggattt etc

33

<210> 22

<211> 1234

<212> PRT

<213> Homo sapiens

<400> 22

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Ala	Ala	Ala	Ile	Met	Ser	Asp	Thr	Asp	Ser	Asp	Glu	Asp	Ser	Ala	Gly
			20					25					30		
Gly	Gly	Pro	Phe	Ser	Leu	Ala	Gly	Phe	Leu	Phe	Gly	Asn	Ile	Asn	Gly
		35					40					45			
Ala	Gly	Gln	Leu	Glu	Gly	Glu	Ser	Val	Leu	Asp	Asp	Glu	Cys	Lys	Lys
	50					55					60				
His	Leu	Ala	Gly	Leu	Gly	Ala	Leu	Gly	Leu	Gly	Ser	Leu	Ile	Thr	Glu
65					70					75					80
Leu	Thr	Ala	Asn	Glu	Leu	Thr	Gly	Thr	Asp	Gly	Ala	Leu	Val	Asn	
			85					90					95		
Asp	Glu	Gly	Trp	Val	Arg	Ser	Thr	Glu	Asp	Ala	Val	Asp	Tyr	Ser	Asp
		100						105					110		
Ile	Asn	Glu	Val	Ala	Glu	Asp	Glu	Ser	Arg	Arg	Tyr	Gln	Gln	Thr	Met
		115					120					125			
Gly	Ser	Leu	Gln	Pro	Leu	Cys	His	Ser	Asp	Tyr	Asp	Glu	Asp	Asp	Tyr
	130					135					140				
Asp	Ala	Asp	Cys	Glu	Asp	Ile	Asp	Cys	Lys	Leu	Met	Pro	Pro	Pro	Pro
145					150					155					160
Pro	Pro	Pro	Gly	Pro	Met	Lys	Lys	Asp	Lys	Asp	Gln	Asp	Ser	Ile	Thr
			165					170						175	
Gly	Glu	Lys	Val	Asp	Phe	Ser	Ser	Ser	Ser	Asp	Ser	Glu	Ser	Glu	Met
		180						185					190		
Gly	Pro	Gln	Glu	Ala	Thr	Gln	Ala	Glu	Ser	Glu	Asp	Gly	Lys	Leu	Thr
	195						200					205			
Leu	Pro	Leu	Ala	Gly	Ile	Met	Gln	His	Asp	Ala	Thr	Lys	Leu	Leu	Pro
	210					215					220				
Ser	Val	Thr	Glu	Leu	Phe	Pro	Glu	Phe	Arg	Pro	Gly	Lys	Val	Leu	Arg
225				230						235					240
Phe	Leu	Arg	Leu	Phe	Gly	Pro	Gly	Lys	Asn	Val	Pro	Ser	Val	Trp	Arg
			245						250					255	
Ser	Ala	Arg	Arg	Lys	Arg	Lys	Lys	Lys	His	Arg	Glu	Leu	Ile	Gln	Glu
		260						265					270		
Glu	Gln	Ile	Gln	Glu	Val	Glu	Cys	Ser	Val	Glu	Ser	Glu	Val	Ser	Gln
	275						280					285			
Lys	Ser	Leu	Trp	Asn	Tyr	Asp	Tyr	Ala	Pro	Pro	Pro	Pro	Pro	Glu	Gln
	290					295					300				
Cys	Leu	Ser	Asp	Asp	Glu	Ile	Thr	Met	Met	Ala	Pro	Val	Glu	Ser	Lys
305					310					315					320
Phe	Ser	Gln	Ser	Thr	Gly	Asp	Ile	Asp	Lys	Val	Thr	Asp	Thr	Lys	Pro
			325					330						335	
Arg	Val	Ala	Glu	Trp	Arg	Tyr	Gly	Pro	Ala	Arg	Leu	Trp	Tyr	Asp	Met
		340						345						350	

Leu	Gly	Val	Pro	Glu	Asp	Gly	Ser	Gly	Phe	Asp	Tyr	Gly	Phe	Lys	Leu	355	360	365
Arg	Lys	Thr	Glu	His	Glu	Pro	Val	Ile	Lys	Ser	Arg	Met	Ile	Glu	Glu	370	375	380
Phe	Arg	Lys	Leu	Glu	Glu	Asn	Asn	Gly	Thr	Asp	Leu	Leu	Ala	Asp	Glu	385	390	395
Asn	Phe	Leu	Met	Val	Thr	Gln	Leu	His	Trp	Glu	Asp	Asp	Ile	Ile	Trp	405	410	415
Asp	Gly	Glu	Asp	Val	Lys	His	Lys	Gly	Thr	Lys	Pro	Gln	Arg	Ala	Ser	420	425	430
Leu	Ala	Gly	Trp	Leu	Pro	Ser	Ser	Met	Thr	Arg	Asn	Ala	Met	Ala	Tyr	435	440	445
Asn	Val	Gln	Gln	Gly	Phe	Ala	Ala	Thr	Leu	Asp	Asp	Asp	Lys	Pro	Trp	450	455	460
Tyr	Ser	Ile	Phe	Pro	Ile	Asp	Asn	Glu	Asp	Leu	Val	Tyr	Gly	Arg	Trp	465	470	475
Glu	Asp	Asn	Ile	Ile	Trp	Asp	Ala	Gln	Ala	Met	Pro	Arg	Leu	Leu	Glu	485	490	495
Pro	Pro	Val	Leu	Thr	Leu	Asp	Pro	Asn	Asp	Glu	Asn	Leu	Ile	Leu	Glu	500	505	510
Ile	Pro	Asp	Glu	Lys	Glu	Glu	Ala	Thr	Ser	Asn	Ser	Pro	Ser	Lys	Glu	515	520	525
Ser	Lys	Lys	Glu	Ser	Ser	Leu	Lys	Lys	Ser	Arg	Ile	Leu	Leu	Gly	Lys	530	535	540
Thr	Gly	Val	Ile	Lys	Glu	Glu	Pro	Gln	Gln	Asn	Met	Ser	Gln	Pro	Glu	545	550	555
Val	Lys	Asp	Pro	Trp	Asn	Leu	Ser	Asn	Asp	Glu	Tyr	Tyr	Tyr	Pro	Lys	565	570	575
Gln	Gln	Gly	Leu	Arg	Gly	Thr	Phe	Gly	Gly	Asn	Ile	Ile	Gln	His	Ser	580	585	590
Ile	Pro	Ala	Val	Glu	Leu	Arg	Gln	Pro	Phe	Phe	Pro	Thr	His	Met	Gly	595	600	605
Pro	Ile	Lys	Leu	Arg	Gln	Phe	His	Arg	Pro	Pro	Leu	Lys	Lys	Tyr	Ser	610	615	620
Phe	Gly	Ala	Leu	Ser	Gln	Pro	Gly	Pro	His	Ser	Val	Gln	Pro	Leu	Leu	625	630	635
Lys	His	Ile	Lys	Lys	Lys	Ala	Lys	Met	Arg	Glu	Gln	Glu	Arg	Gln	Ala	645	650	655
Ser	Gly	Gly	Gly	Glu	Met	Phe	Phe	Met	Arg	Thr	Pro	Gln	Asp	Leu	Thr	660	665	670
Gly	Lys	Asp	Gly	Asp	Leu	Ile	Leu	Ala	Glu	Tyr	Ser	Glu	Glu	Asn	Gly	675	680	685
Pro	Leu	Met	Met	Gln	Val	Gly	Met	Ala	Thr	Lys	Ile	Lys	Asn	Tyr	Tyr	690	695	700
Lys	Arg	Lys	Pro	Gly	Lys	Asp	Pro	Gly	Ala	Pro	Asp	Cys	Lys	Tyr	Gly	705	710	715
Glu	Thr	Val	Tyr	Cys	His	Thr	Ser	Pro	Phe	Leu	Gly	Ser	Leu	His	Pro	725	730	735
Gly	Gln	Leu	Leu	Gln	Ala	Phe	Glu	Asn	Asn	Leu	Phe	Arg	Ala	Pro	Ile	740	745	750
Tyr	Leu	His	Lys	Met	Pro	Glu	Thr	Asp	Phe	Leu	Ile	Ile	Arg	Thr	Arg	755	760	765
Gln	Gly	Tyr	Tyr	Ile	Arg	Glu	Leu	Val	Asp	Ile	Phe	Val	Val	Gly	Gln	770	775	780
Gln	Cys	Pro	Leu	Phe	Glu	Val	Pro	Gly	Pro	Asn	Ser	Lys	Arg	Ala	Asn	785	790	795
Thr	His	Ile	Arg	Asp	Phe	Leu	Gln	Val	Phe	Ile	Tyr	Arg	Leu	Phe	Trp			

				805					810				815				
Lys	Ser	Lys	Asp	Arg	Pro	Arg	Arg	Ile	Arg	Met	Glu	Asp	Ile	Lys	Lys		
			820					825					830				
Ala	Phe	Pro	Ser	His	Ser	Glu	Ser	Ser	Ile	Arg	Lys	Arg	Leu	Lys	Leu		
		835					840					845					
Cys	Ala	Asp	Phe	Lys	Arg	Thr	Gly	Met	Asp	Ser	Asn	Trp	Trp	Val	Leu		
	850					855					860						
Lys	Ser	Asp	Phe	Arg	Leu	Pro	Thr	Glu	Glu	Glu	Ile	Arg	Ala	Met	Val		
865					870					875					880		
Ser	Pro	Glu	Gln	Cys	Ala	Tyr	Tyr	Ser	Met	Ile	Ala	Ala	Glu	Gln			
			885					890					895				
Arg	Leu	Lys	Asp	Ala	Gly	Tyr	Gly	Glu	Lys	Ser	Phe	Phe	Ala	Pro	Glu		
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Glu	Glu	Asn	Glu	Glu	Asp	Phe	Gln	Met	Lys	Ile	Asp	Asp	Glu	Val	Arg		
	915						920					925					
Thr	Ala	Pro	Trp	Asn	Thr	Thr	Arg	Ala	Phe	Ile	Ala	Ala	Met	Lys	Gly		
	930					935					940						
Lys	Cys	Leu	Leu	Glu	Val	Thr	Gly	Val	Ala	Asp	Pro	Thr	Gly	Cys	Gly		
945					950					955					960		
Glu	Gly	Phe	Ser	Tyr	Val	Lys	Ile	Pro	Asn	Lys	Pro	Thr	Gln	Gln	Lys		
			965					970					975				
Asp	Asp	Lys	Glu	Pro	Gln	Pro	Val	Lys	Lys	Thr	Val	Thr	Gly	Thr	Asp		
	980							985					990				
Ala	Asp	Leu	Arg	Arg	Leu	Ser	Leu	Lys	Asn	Ala	Lys	Gln	Leu	Leu	Arg		
	995						1000					1005					
Lys	Phe	Gly	Val	Pro	Glu	Glu	Glu	Ile	Lys	Lys	Leu	Ser	Arg	Trp	Glu		
	1010					1015					1020						
Val	Ile	Asp	Val	Val	Arg	Thr	Met	Ser	Thr	Glu	Gln	Ala	Arg	Ser	Gly		
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Glu	Gly	Pro	Met	Ser	Lys	Phe	Ala	Arg	Gly	Ser	Arg	Phe	Ser	Val	Ala		
			1045					1050					1055				
Glu	His	Gln	Glu	Arg	Tyr	Lys	Glu	Glu	Cys	Gln	Arg	Ile	Phe	Asp	Leu		
		1060					1065					1070					
Gln	Asn	Lys	Val	Leu	Ser	Ser	Thr	Glu	Val	Leu	Ser	Thr	Asp	Thr	Asp		
	1075					1080					1085						
Ser	Ser	Ser	Ala	Glu	Asp	Ser	Asp	Phe	Glu	Glu	Met	Gly	Lys	Asn	Ile		
	1090				1095						1100						
Glu	Asn	Met	Leu	Gln	Asn	Lys	Lys	Thr	Ser	Ser	Gln	Leu	Ser	Arg	Glu		
1105				1110				1115						1120			
Arg	Glu	Glu	Gln	Glu	Arg	Lys	Glu	Leu	Gln	Arg	Met	Leu	Leu	Ala	Ala		
		1125						1130						1135			
Gly	Ser	Ala	Ala	Ser	Gly	Asn	Asn	His	Arg	Asp	Asp	Asp	Thr	Ala	Ser		
		1140						1145					1150				
Val	Thr	Ser	Leu	Asn	Ser	Ser	Ala	Thr	Gly	Arg	Cys	Leu	Lys	Ile	Tyr		
	1155					1160					1165						
Arg	Thr	Phe	Arg	Asp	Glu	Glu	Gly	Lys	Glu	Tyr	Val	Arg	Cys	Glu	Thr		
	1170				1175					1180							
Val	Arg	Lys	Pro	Ala	Val	Ile	Asp	Ala	Tyr	Val	Arg	Ile	Arg	Thr	Thr		
1185				1190					1195						1200		
Lys	Asp	Glu	Glu	Phe	Ile	Arg	Lys	Phe	Ala	Leu	Phe	Asp	Glu	Gln	His		
		1205						1210					1215				
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Arg	Leu																

<210> 23

<211> 52

<212> DNA
 <213> Artificial Sequence

 <220>
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 acgcgtcgac atgcatcatc atcatcatca tatggaggat ctaccaggg at 52

 <210> 24
 <211> 38
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 <213> Artificial Sequence

 <220>
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 <400> 24
 atagttagcg gccgcacact gctggtgtca accaaca 38

 <210> 25
 <211> 52
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Homo sapiens oligonucleotide

 <400> 25
 acgcgtcgac atgcatcatc atcatcatca tatgggaccc ggctgcgatt tg 52

 <210> 26
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 <400> 26
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 <210> 27
 <211> 31
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 <400> 27
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 <210> 28
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Homo sapiens oligonucleotide

<400> 28

ccggtacctt cccgatgttg ttcacaaaa ag

32

<210> 29

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 29

acgcgtcgac atccaagttc aagttgtctg

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<210> 30

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 30

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<211> 41

<212> DNA

<213> Artificial Sequence

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aaaactgcag cgcggtaccg cgtgcaggtg acgttattgg a

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<210> 32

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 32

atagtttagc ggccgccttg tgacaagaag tgacac

36

*201
conclude*